

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/768,840DATE: 03/15/2001  
TIME: 22:39:47

INPUT SET: S36517.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information  
4  
5 (i) APPLICANT: Hillman, Jennifer L.  
6 Goli, Surya K.  
7  
8 (ii) TITLE OF THE INVENTION: NOVEL CALCIUM-BINDING  
9 PROTEIN  
10  
11 (iii) NUMBER OF SEQUENCES: 4  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
15 (B) STREET: 3174 Porter Drive  
16 (C) CITY: Palo Alto  
17 (D) STATE: CA  
18 (E) COUNTRY: USA  
19 (F) ZIP: 94304  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Diskette  
23 (B) COMPUTER: IBM Compatible  
24 (C) OPERATING SYSTEM: DOS  
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: 09/768,840  
29 (B) FILING DATE:  
30 (C) CLASSIFICATION:  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: 09/206,499  
34 (B) FILING DATE:  
35  
36 (viii) ATTORNEY/AGENT INFORMATION:  
37 (A) NAME: Billings, Lucy J.  
38 (B) REGISTRATION NUMBER: 36,749  
39 (C) REFERENCE/DOCKET NUMBER: PF-0261 US  
40  
41 (ix) TELECOMMUNICATION INFORMATION:  
42 (A) TELEPHONE: 415-855-0555  
43 (B) TELEFAX: 415-845-4166  
44  
45  
46 (2) INFORMATION FOR SEQ ID NO:1:

# 2

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48

(i) SEQUENCE CHARACTERISTICS:

49

(A) LENGTH: 328 amino acids

50

(B) TYPE: amino acid

51

(C) STRANDEDNESS: single

52

(D) TOPOLOGY: linear

53

54

(vii) IMMEDIATE SOURCE:

55

(A) LIBRARY: CONUTUT01

56

(B) CLONE: 2509570

57

58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

59

60

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His

61

1 5 10 15

62

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly

63

20 25 30

64

Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala

65

35 40 45

66

His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val

67

50 55 60

68

Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu

69

65 70 75 80

70

Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp

71

85 90 95

72

Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg

73

100 105 110

74

His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp

75

115 120 125

76

Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly

77

130 135 140

78

His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr

79

145 150 155 160

80

Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp

81

165 170 175

82

Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu

83

180 185 190

84

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr

85

195 200 205

86

Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu

87

210 215 220

88

Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala

89

225 230 235 240

90

Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn

91

245 250 255

92

Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro

93

260 265 270

94

Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu

95

275 280 285

96

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly

97

290 295 300

98

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp

99

305 310 315 320

**INPUT SET: S36517.raw**

100      Leu Thr Arg His His Asp Glu Leu  
101                          325

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 1055 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: CONTUT01

(B) CLONE: 2509570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 1262329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

149
150 Met Ala Arg Gly Gly Arg Gly Arg Arg Leu Gly Leu Ala Leu Gly Leu
151 1 5 10 15
152 Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr

```

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```

153          20          25          30
154 Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg
155          35          40          45
156 Pro Pro Glu Asp Asn Gln Ser Phe Gln Tyr Asp His Glu Ala Phe Leu
157          50          55          60
158 Gly Lys Glu Asp Ser Lys Thr Phe Asp Gln Leu Thr Pro Asp Glu Ser
159          65          70          75          80
160 Lys Glu Arg Leu Gly Lys Ile Val Asp Arg Ile Asp Asn Asp Gly Asp
161          85          90          95
162 Gly Phe Val Thr Thr Glu Glu Leu Lys Thr Trp Ile Lys Arg Val Gln
163          100          105          110
164 Lys Arg Tyr Ile Phe Asp Asn Val Ala Lys Val Trp Lys Asp Tyr Asp
165          115          120          125
166 Arg Asp Lys Asp Asp Lys Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr
167          130          135          140
168 Tyr Gly Tyr Tyr Leu Gly Asn Pro Ala Glu Phe His Asp Ser Ser Asp
169          145          150          155          160
170 His His Thr Phe Lys Lys Met Leu Pro Arg Asp Glu Arg Arg Phe Lys
171          165          170          175
172 Ala Ala Asp Leu Asn Gly Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr
173          180          185          190
174 Ala Phe Leu His Pro Glu Glu Phe Glu His Met Lys Glu Ile Val Val
175          195          200          205
176 Leu Glu Thr Leu Glu Asp Ile Asp Lys Asn Gly Asp Gly Phe Val Asp
177          210          215          220
178 Gln Asp Glu Tyr Ile Ala Asp Met Phe Ser His Glu Glu Asn Gly Pro
179          225          230          235          240
180 Glu Pro Asp Trp Val Leu Ser Glu Arg Glu Gln Phe Asn Glu Phe Arg
181          245          250          255
182 Asp Leu Asn Lys Asp Gly Lys Leu Asp Lys Asp Glu Ile Arg His Trp
183          260          265          270
184 Ile Leu Pro Gln Asp Tyr Asp His Ala Gln Ala Glu Ala Arg His Leu
185          275          280          285
186 Val Tyr Glu Ser Asp Lys Asn Lys Asp Glu Lys Leu Thr Lys Glu Glu
187          290          295          300
188 Ile Leu Glu Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr
189          305          310          315          320
190 Gly Glu Asp Leu Thr Lys Asn His Asp Glu Leu
191          325          330

```

## (2) INFORMATION FOR SEQ ID NO:4:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 220582

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

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206  
207 Met Ala Arg Gly Gly Arg Leu Gly Leu Ala Leu Gly Leu Leu Leu Ala  
208 1 5 10 15  
209 Leu Val Leu Ala Leu Arg Ala Lys Pro Thr Val Arg Lys Glu Arg Val  
210 20 25 30  
211 Val Arg Pro Asp Ser Glu Leu Gly Glu Arg Pro Pro Glu Asp Asn Gln  
212 35 40 45  
213 Ser Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Lys Glu Asp Ser Lys  
214 50 55 60  
215 Thr Phe Asp Gln Leu Ser Pro Asp Glu Ser Lys Glu Arg Leu Gly Lys  
216 65 70 75 80  
217 Ile Val Asp Arg Ile Asp Ser Asp Gly Asp Gly Leu Val Thr Thr Glu  
218 85 90 95  
219 Glu Leu Lys Leu Trp Ile Lys Arg Val Gln Lys Arg Tyr Ile Tyr Asp  
220 100 105 110  
221 Asn Val Ala Lys Val Trp Lys Asp Tyr Asp Arg Asp Lys Asp Glu Lys  
222 115 120 125  
223 Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr Tyr Gly Tyr Tyr Leu Gly  
224 130 135 140  
225 Asn Pro Ala Glu Phe His Asp Ser Ser Asp His His Thr Phe Lys Lys  
226 145 150 155 160  
227 Met Leu Pro Arg Asp Glu Arg Arg Phe Lys Ala Ser Asp Leu Asp Gly  
228 165 170 175  
229 Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr Ala Phe Leu His Pro Glu  
230 180 185 190  
231 Glu Phe Glu His Met Lys Glu Ile Val Val Leu Glu Thr Leu Glu Asp  
232 195 200 205  
233 Ile Asp Lys Asn Gly Asp Gly Phe Val Asp Gln Asp Glu Tyr Ile Ala  
234 210 215 220  
235 Asp Met Phe Ser His Glu Asp Asn Gly Pro Glu Pro Asp Trp Val Leu  
236 225 230 235 240  
237 Ser Glu Arg Glu Gln Phe Asn Asp Phe Arg Asp Leu Asn Lys Asp Gly  
238 245 250 255  
239 Lys Leu Asp Lys Asp Glu Ile Arg His Trp Ile Leu Pro Gln Asp Tyr  
240 260 265 270  
241 Asp His Ala Gln Ala Glu Ala Arg His Leu Val Tyr Glu Ser Asp Lys  
242 275 280 285  
243 Asn Lys Asp Glu Met Leu Thr Lys Glu Glu Ile Leu Asp Asn Trp Asn  
244 290 295 300  
245 Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp Leu Thr Lys  
246 305 310 315 320  
247 Asn His Asp Glu Leu  
248 325  
249

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/768,840**

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*INPUT SET: S36517.raw*

Line

Error

Original Text